

# Retinopathy - Sequential Logit Models

August 21, 2024

```
> library(catdata)
> data(retinopathy)
```

For sequential models again the "vglm"-function from the "VGAM"-library is needed, but now family option "sratio" is required.

```
> library(VGAM)
```

Now several sequential logit models are fitted and compared by their corresponding deviances. The first model is the sequential logit model with all category-specific effects, so the option "parallel=FALSE" is used.

```
> seqm1 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE), data = retinopathy)
> deviance(seqm1)
```

```
[1] 891.4193
```

No category-specific effect for DIAB:

```
> seqm2 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE ~ SM + GH + BP), data = retinopathy)
> deviance(seqm2)
```

```
[1] 891.4428
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm2)-deviance(seqm1), df=1)
```

```
[1] 0.8781324
```

No category-specific effect for GH:

```
> seqm3 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE ~ SM + BP), data = retinopathy)
> deviance(seqm3)
```

```
[1] 891.4689
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm3)-deviance(seqm2), df=1)
```

```
[1] 0.8716468
```

No category-specific effect for BP:

```
> seqm4 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=FALSE ~ SM), data = retinopathy)
> deviance(seqm4)
```

```
[1] 891.9767
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm4)-deviance(seqm3), df=1)
```

```
[1] 0.4760739
```

No category-specific effect for GH (only global effects):

```
> seqm5 <- vglm(RET ~ SM + DIAB + GH + BP, family = sratio (link="logit",
+ parallel=TRUE), data = retinopathy)
> deviance(seqm5)
```

```
[1] 897.7104
```

Testing the removed effect:

```
> 1-pchisq(deviance(seqm5)-deviance(seqm4), df=1)
```

```
[1] 0.01664239
```

As the last test is significant, model "seqm4" is analyzed in detail.

```
> summary(seqm4)
```

Call:

```
vglm(formula = RET ~ SM + DIAB + GH + BP, family = sratio(link = "logit",
parallel = FALSE ~ SM), data = retinopathy)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept):1	11.12783	1.16861	9.522	< 2e-16 ***
(Intercept):2	10.91554	1.21342	8.996	< 2e-16 ***
SM:1	-0.37755	0.20248	-1.865	0.0622 .
SM:2	0.49077	0.31285	1.569	0.1167
DIAB	-0.12823	0.01229	-10.430	< 2e-16 ***
GH	-0.42480	0.06730	-6.312	2.76e-10 ***
BP	-0.06227	0.01220	-5.104	3.33e-07 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Names of linear predictors: logitlink(P[Y=1|Y>=1]), logitlink(P[Y=2|Y>=2])

Residual deviance: 891.9767 on 1219 degrees of freedom

Log-likelihood: -445.9884 on 1219 degrees of freedom

Number of Fisher scoring iterations: 6

Warning: Hauck-Donner effect detected in the following estimate(s):  
'(Intercept):1'

Exponentiated coefficients:

	SM:1	SM:2	DIAB	GH	BP
	0.6855376	1.6335785	0.8796526	0.6539010	0.9396286

The summary gives no p-values for the individual covariates, they have to be computed separately. For this purpose the t-values are copied from the summary. The quadratic t-values are the wald-statistics which can be used to produce the individual p-values.

p-value intercept1:

```
> 1 - pchisq(9.5223^2, df=1)
```

```
[1] 0
```

p-value intercept2:

```
> 1 - pchisq(8.9957^2, df=1)
```

```
[1] 0
```

p-value SM1:

```
> 1 - pchisq((-1.8646)^2, df=1)
```

```
[1] 0.06223749
```

p-value SM2:

```
> 1 - pchisq(1.5687^2, df=1)
```

```
[1] 0.1167179
```

p-value DIAB:

```
> 1 - pchisq((-10.4303)^2, df=1)
```

```
[1] 0
```

p-value GH:

```
> 1 - pchisq((-6.3116)^2, df=1)
```

```
[1] 2.761653e-10
```

p-value BP:

```
> 1 - pchisq((-5.1037)^2, df=1)
```

```
[1] 3.330761e-07
```

To receive the corresponding odds-ratios, the following command can be used.

```
> exp(coefficients(seqm4)[3:7])
```

SM:1	SM:2	DIAB	GH	BP
0.6855376	1.6335785	0.8796526	0.6539010	0.9396286